

N-TERMINAL AMINOACID SEQUENCES

Position	A	B	C
01			LEU
02			ALA
03			VAL
04			PRO
05		ALA	ALA
06		SER	SER
07		---	ARG
08	----**	---	ASN
09	GLN	GLN	GLN
10	SER	SER	SER
11	SER	SER	SER
12	---	---	GLY
13	ASP	ASP	ASP
14	THR	THR	THR
15	VAL	VAL	VAL
16	ASP	ASP	ASP
17	GLN	GLN	
18		GLY	
19		TYR	
20		GLN	
21		ARG	
22		PHE	
23		SER	
24		GLU	
25		THR	
26		SER	
27		HIS	
28		LEU	
29		ARG	
30		(GLY)*	
31		GLN	
32		TYR	
33		ALA	
34		PRO	
35		PHE	
36		PHE	
37		(ASP)	
38		LEU	
39		ALA	

Figure 1a

PEPTIDE AMINOACID SEQUENCES

	A	B	C	D	E
Position					
01	GLN	(TRP)*	MET	ALA	VAL
02	----**	SER	MET	SER	VAL
03	GLN	PHE	GLN	SER	ASP
04	ALA	ASP	CYS	ALA	----
05	GLU	THR	GLN	GLU	ARG
06	GLN	ILE	ALA	LYS	PHE
07	GLU	SER	GLU	GLY	PRO
08	PRO	THR	GLN	TYR	TYR
09	LEU	SER	GLU	ASP	THR
10	VAL	THR	PRO	LEU	GLY
11	(ARG)	VAL	LEU	VAL	----
12	VAL	ASP	VAL	VAL	ALA
13	LEU	THR	ARG		
14	VAL	LYS	VAL		
15	ASN	LEU	LEU		
16	(ASP)	SER	VAL		
17	(ARG)	PRO	ASN		
18	(VAL)	PHE	ASP		
19	VAL	(CYS)	ARG		
20	PRO	(ASP)			
21		LEU			
22		PHE			
23		THR			

Figure 1b

N-TERMINUS 100KD PROTEIN

Position

01	VAL
02	VAL
03	ASP
04	GLU
05	ARG
06	PHE
07	PRO
08	TYR
09	THR
10	GLY

Figure 1c

206120" 60/6/001

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
 Peptide C: Leu-Ala-Val-Pro-Ala-Ser-Arg-Asn-Gln-Ser-Ser-Gly-Asp-Thr-Val-Asp
 Peptide B: Ala-Ser-****-Gln-Ser-Ser-****-Asp-Thr-Val Asp-Gln-Gly-Tyr-Gln-
 Peptide A: ****-Gln-Ser-Ser-****-Asp-Thr-Val-Asp-Gln

Possible

codons: 5' CTG-GCG-GTG-CCG-GCG-TCG-CCG-AAT-CAA-TCG-TCG-GGG-GAT-ACG-GTG-GAT-CAA-GGG-TAT-CAA-
 A A A A A A A C G A A A C A A C G A C G
 T T T T T T T T T T T T T T T
 C C C C C C C C C C C C C C C
 TTA AGT AGA AGT AGT
 G C G C C

—AB1024: 3'-CGG-CAG-GGG-CGG-TCG-GCG-TTG-GTC-TCG-CCG-CTG-TGG-CAG-CTG-GTC

AB1065: 3'-CCG-CTG-TGG-CAC-CTG-GTC A

AB1066: A G

AB1067: A

AB1068: A

AB1069: A

AB1070: A A A G A

AB1226: 3'-CAG-CTG-GTC-CCG-ATG-GTC C A A

AB1227: 3'-CAG-CTG-GTC-CCG-ATG-GTC C A T A A T

AB1298: 3'-CTG-TGG-CAG-CTG-GTC-CCG-ATG-GTC A C C A T C A T

Figure 2a (sheet 1 of 2)

206120" 60/6/001

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

Peptide A: (Gln- ? -Gln-Ala-Glu-Gln-Glu-Pro-Leu-Val-(Ser/Arg)-Val-Leu-Val-(Asp/Asn)

CAG-???-CAG-GCG-GAG-CAG-GAG-CCG-CTG-GTG-(TCG/CGG)-GTG-CTG-GTG-(GAT/AAT)

A	A	A	A	A	A	A	A	A	A	A	A	A	A	C
				T					T	T	T	T	T	T
				C					C	C	C	C	C	C
								TTG	AGT	AGG	TTG			
								A	C		A			

AB1295:

3'-GTC.CGC.CTC.GTC.CTC.GGG.GAG.CA-5'

T G T T T C A C

16 17 18 19 20 21 22

-Asp/Thr/Arg-(Arg/Val)-Val-Pro-(Pro)-Met-Gly

-GAT/ACG/CGG-(CGG/GTG)-GTG-CCG-(CCG)-ATG-GGG

C	A	A	A	A	A	A	A
		T	T	T	T	T	T
		C	C	C	C	C	C
AGG	AGG						
A	A						

Figure 2b (sheet 1 of 2)

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
 Peptide B: (Trp)-Ser-Phe-Asp-Thr-Ile-Ser-Thr-Ser-Thr-Val-Asp-Thr-Lys-Leu-Ser-Pro-Phe-

(TGG)-TCG-TTT-GAT-ACG-ATA-TCG-ACG-TCG-ACG-GTG-GAT-ACG-AAG-CTG-TCG-CCG-TTT-
 A C C A T A A A A C A A A A A C
 T C T T T T T T T T T T T T T
 C C C C C C C C C C C C C C C
 AGT AGT AGT AGT AGT AGT AGT AGT AGT AGT AGT AGT AGT AGT
 C C C C C C C C C C C C C C C

AB1296 : 3'-AAG. CTG. TGC. TAG. AGG. TGG. AGG. TGG. CAC. CTG. TGC. TTC-5'
 TCC C TCC C AB1297: 3'-GGC.AAG.
 G

19 20 21 22 23 24 25 26 27 28 29 30 31 32 33
 (Cys)-(Asp)-Leu-Phe-Thr-(Thr)-(Asp)-(Glu)-(Cys)-(Ile)-(Thr/Asn)-(Tyr)-(Arg/Gly)-(Tyr)-Leu

(GTG)-(GAT)- CTG- TTT- ACG-(ACG)-(GAT)- GAG) - (TGT)-(ATA)-(ACG/AAT) - (TAT)-(CGG/GGG)-(TAT)-CTG
 C C A C A A C A A C T A C C A A A C A
 T T T T C T C T T T T T T T T
 C C C C C C C C C C C C C C C
 TTG A AGG A TTG A

(ACG). (CTG). GAG. AAG. TGC. (TGC). (CTG). (CTC). (ACG).(TAG). (T)-5'
 C G G

Figure 2b (sheet 2 of 2)

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
Phe-Ser-Tyr-Gly-Ala-Ala-Ile-Pro-Gln-Ser-Thr-Gln-Glu-Lys-Gln-Phe-Ser-Gln-Glu-Phe-Arg-Asp-Gly

[illegible]

AB1025: 3'-ATG-CCG-CGG-CGG-TAG-GGG-GTC-TCG-TGG-GTC-CTC-TTC-GTC-AAG-TCG-GTC-CTC-AAG-GC-5
AB1026: 3'-GTC-CTC-TTC-GTC-AAG-TCG-GTC-CTC-AAG-GC-5

AB1027: 3'-ATG-CCG-GCG-CGC-TAA-GGC-GTC-5'

Figure 3

206T20" 60/6/00T

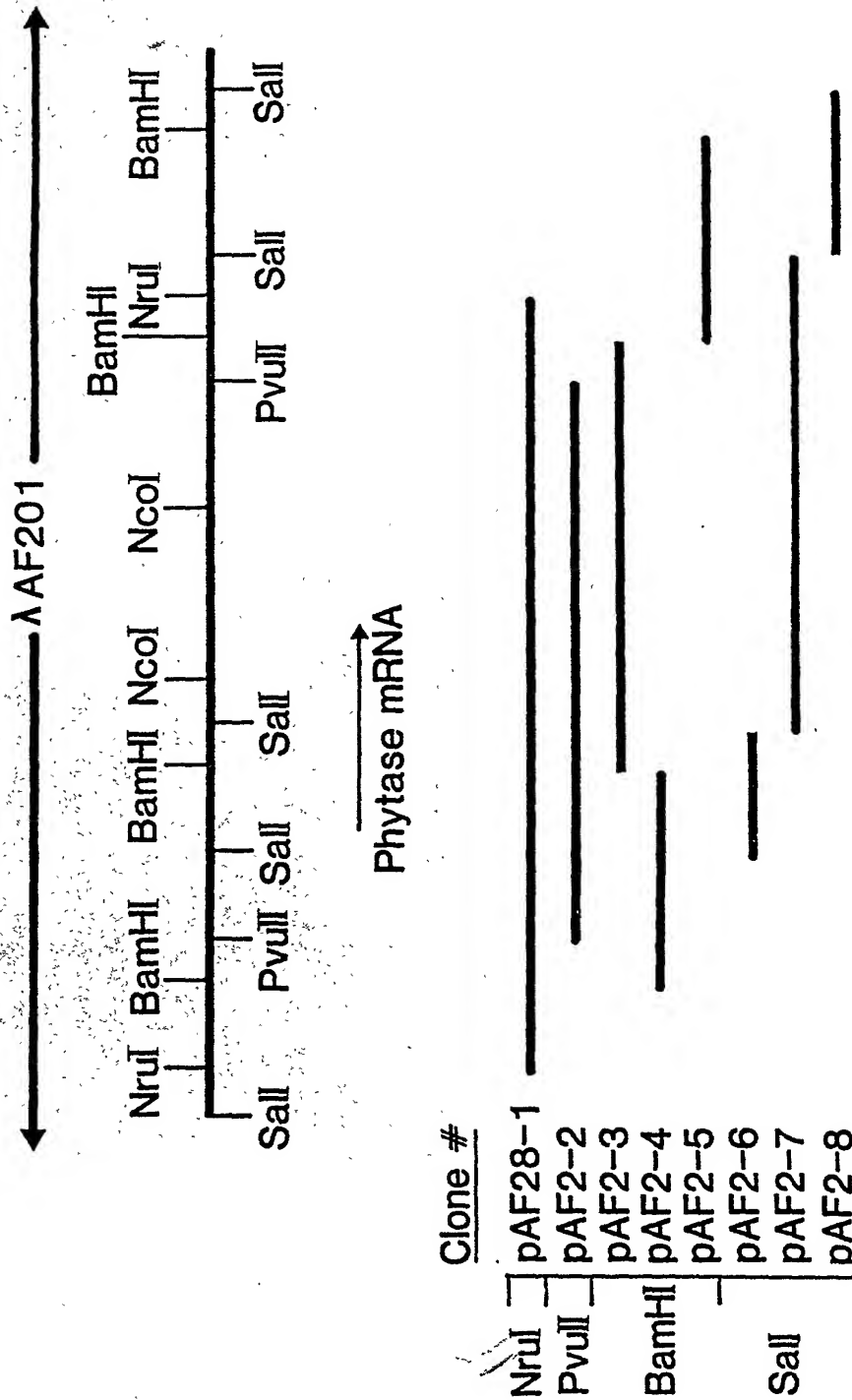


Figure 4

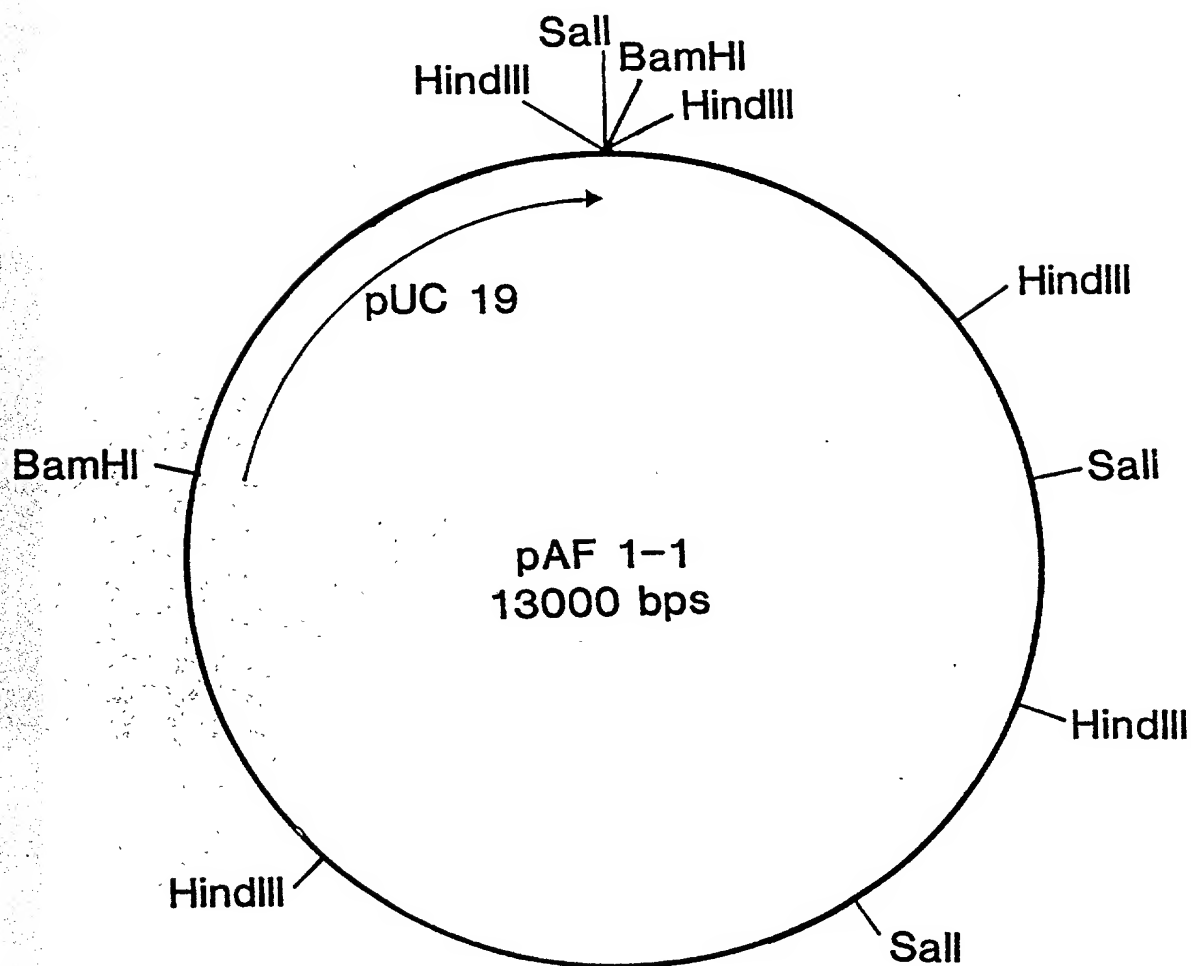


Figure 5

Figure 6 (sheet 1 of 7)

GTCGACTTCCCGTCCTATTCTGGCCTCGTCCGCTGAAGATCCATCCCACCA
 Sali
 TTGCACGTGGGCCACCTTTGTGAGCTTCTAACCTGAACTGGTAGAGTATC 100
 ACACACCATGCCAAGGTGGGATGAAGGGGTATATGAGACCGTCCGGTCC
 GGCGCGATGGCCGTAGCTGCCACTCGCTGCTGTGCAAGAAATTACTTCTC 200
 ATAGGCATCATGGGCGTCTCTGCTGTTCTACTTCCTTTGTATCTCCTGTC
 translation start
TGGGTATGCTAAGCACCACAATCAAAGTCTAATAAGGACCCTCCCTTCCG
 start<-----
AGGGCCCCTGAAGCTCGGACTGTGTGGGACTACTGATCGCTGACTATCTG
 ---intron---
TGCAGAGTCACCTCCGGACTGGCAGTCCCCGCCTCGAGAAATCAATCCAG
 ->end 400
 TTGCGATACGGTCGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATC 414
 TTTGGGGTCAATACGCACCGTTCTTCTCTCTGGCAAACGAATCGGTCATC 500
 TCCCCTGAGGTGCCCGCCGGATGCAGAGTCACTTTCGCTCAGGTCCTCTC
 CCGTCATGGAGCGCGGTATCCGACCGACTCCAAGGGCAAGAAATACTCCG 600
 CTCTCATTGAGGAGATCCAGCAGAACGCGACCACCTTTGACGGAAAATAT
 GCCTTCCTGAAGACATACTACAGCTTGGGTGCAGATGACCTGACTCC 700
 CTTCCGAGAACAGGAGCTAGTCAACTCCGGCATCAAGTTCTACCAGCGGT
 ACGAATCGCTCACAAGGAACATCGTTCCATTATCCGATCCTCTGGCTCC 800
 AGCCGCGTGATCGCCTCCGGCAAGAAATTGATCGAGGGCTTCCAGAGCAC
 CAAGCTGAAGGATCCCTCGTGCCCGAGCCCGGCCAATCGTCGCCCAAGATCG 900
 BamHI
 ACGTGGTCATTTCCGAGGCCAGCTCATCCAACAACACTCTCGACCCAGGC 865
 ACCTGCACTGTCTTCTGAAGACAGCGAATTGGCCGATACCGTCGAAGCCAA 1000

414
 90
 504
 865
 865
 174

205120 60767001

Figure 6 (sheet 2 of 7)

TTTCACCGCCACGTTTCGTCCCCTCCATTTCGTCAACGTCTGGAGAACGACC
TGTCGGGTGTGACTCTCACAGACACAGAAGTGACCTACCTCATGGACATG 1100
TGCTCCTTCGACACCATCTCCACCAGCACCGTCGACACCAAGCTGTCCCC
Sall
CTTCTGTGACCTGTTCACCCATGACGAATGGATCAACTACGACTACCTCC 1200
AGTCCTTGAAAAAGTATTACGGCCATGGTGACGGTAACCCGCTCGGCCCG
ACCCAGGGCGTCGGCTACGCTAACGAGCTCATCGCCCGTCTGACCCACTC 1300
GCCTGTCCACGATGACACCAGTTCCAACCACACTTTGGACTCGAGCCCGG
CTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTTTCGCATGACAAC 1400
GGCATCATCTCCATTCTCTTTGCTTTAGGTCTGTACAACGGCACTAAGCC
GCTATCTACCACGACCGTGGAGAATATCACCCAGACAGATGGATTCTCGT 1500
CTGCTTGGACGGTTCCGTTTGCTTCGCGTTTGTACGTCGAGATGATGCAG
TGTCAGGCGGAGCAGGAGCCGCTGGTCCGTGTCTTGGTTAATGATCGCGT 1600
TGTCCCGCTGCATGGGTGTCCGTTGATGCTTTGGGGAGATGTACCCGGG
ATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGGGGTGATTGGGCG 1700
GAGTGTTTGTGCTTAGCTGAATTACCTTGATGAATGGTATGTATCACATTG
translation stop
CATATCATTAGCACTTCAGGTATGTATTATCGAAGATGTATATCGAAAGG 1800
ATCAATGGTGACTGTCACTGGTTATCTGAATATCCCTCTATACCTCGTCC
CACAACCAATCATCACCCCTTTAAACAATCACACTCAACGCACAGCGTACA 1900
AACGAACAAACGCACAAAGAATATTTTACACTCCTCCCCAACGCAATACC
AACCGCAATTCATCATACCTCATATAAATACAATACAATACAATACATCC 2000

Figure 6 (sheet 3 of 7)

ATCCCTACCCTCAAGTCCACCCATCCTATAATCAATCCCTACTTACTTAC
TTCTCCCCCTCCCCCTCACCTTCCCAGAACTACCCCCGAAGTAGTAAT 2100
AGTAGTAGTAGAAGAAGCAGACGACCTCTCCACCAATCTCTTCGGCCTCT
TATCCCCATACGCTACACAAAACCCCCACCCGTTAGCATGCACTCAGAA 2200
AATAATCAAAAATAACTAAGAAGGAAAAAAGAAGAAGAAAGGTTACAT
ACTCCTCTCATACAACTCCAAGACGTATACATCAAGATGGGCAATCCCA 2300
CCATTACTGATATCCATCTATGAACCCATTCCCATCCCACGTTAGTTGAT
TACTTTACTTAGAAGAAGAAAAGGGAAGGGAAGGGAAGAAAGTGGATGG 2400
GATTGAGTTAGTGCTCACCGTCTCGCAGCAAGTTTATATTCTTTTGTGTTG
GCGGATATCTTTCCTGCTCCTGCTGGACGTTGTACGGGGTGGTAGTGG 2500
TTGGCGGTGGTGAGGGTCCATGATCACTCTTGGTTTGGGGGGTTGTTGTT
GTCGTTGTTGTTGTTGTTGGGTGGGCATTTTCTTTTCTTCACTGGGGAT 2600
TATTATTGGAATTGGTTAGTTTGAGTGAGTGGGTAATATTGAATGGGTG
ATTATTGGGAATGAAGTAGATTTGGCTATGAATGGTTGATGGGATGGAAT 2700
GAATGGATGGATGAATAGATGGAGGCGGAAAAGTCAGGTGGTTTGAGGTT
CGGATTATTATCTTTGTGCCTGAGGCATCACTCTCCATCTATGTTGTTCT 2800
TTCTATACCGATCTACCAGAGCTAAGTTGACTGATTCTACACAGTGCAC
AATAAGTATGTACTTATTTCAATTTAGAGTATTTAGATTAACCCGCTGTGC 2900
TATTTGCCGTAGCTTTCCACCCAATTTGGAAGTTCGAAGAATTAAAACTC
ATCCTACAGTACAGAATAGAAGTAAAAGGAGAAGAGAAAAACAAGATAAT 3000

Figure 6 (sheet 4 of 7)

ACAACCAGTCCAGGTCCATTCTAGATCTCGAATGACCACCAAATAAGAAA
GCAACAAGCAAGTAAGCAAAGCATAAGTCTAAATGAACGCCAATAACTTC 3100
ATCGCCTGCCTTTGAAACTGAACGCTATGCACGAATGGCTCGAAATGATT
CCCTTAACTCCGTAGTATTGAGAGTGAGAGGAAAAGAAAAAAGAGACAG 3200
AAAAGCTGACCATGGGAAAGAAGCATGATCAGTCGGGAATGGATCTGCGG
GTTGAGATAGATATGAGTTGCCTCGCAGATCCGGTGACAAGATAAGAGAA 3300
TTGGGAGATGTGATCAGCCACTGTAACCTCATCAAGCATCGACATTCAAC
GGTCGGGTCTGCGGGTTGAGATGCAAGTTGAGATGCCACGCAGACCCGAA 3400
CAGAGTGAGAGATGTGAGACTTTTGAACCACTGTGACTTCATCAAGCATC
AAAACACACTCCATGGTCAATCGGTTAGGGTGTGAGGGTTGATATGCCAG 3500
GTTGATGCCACGCAGACCCGAACCGACTGAGAAATATGAAAAGTTGGAC
AGCCACTTCATCTTCATCAAGCGTAAAACCCCAATCAATGGTAAATCGAA 3600
AACGAATCTGCGGGCTGATGTGGAAATGAGACGAATGCCTCGCAGATTCTG
AAGACACGTAAATCGAGATGAACAATCACTTTAACTTCATCAAAGCCTTA 3700
AATCACCCAATGGCCAGTCTATTCGGGTCTGCGGGTTGAGGTTCTGTTG
AGATGCCACGCAGACTGCGAACATGCGATGCATTATAAGTTGGACGAGTG 3800
TAGACTGACCATTGATAACCGAGATAAACAATCACTTCAACTTCATCAA
GCCTTAAATCACTCAATGGCCAGTCTGTTTGCGGTCTGCGGGCTGATACC 3900
CAAGTTGCGATGCCACGCAGACTGCAAACATTGATCGAGAGACGAGAAAA
ACAACGCACTTTAACTTCAACAAAAGCCTTTCAATCAGTCAATGGCCAGT 4000

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Figure 6 (sheet 5 of 7)

CTGTTGCGGGTCTGCGGGCTGATATGCGAGTTGAGGTGCCTCGCAGACCG
CGAACATGCGATGTAATTTCTTAGTTAGACGAGTGCCTGGCCATTGAGAA 4100
ACGAGAGAAACAACCACTTTAACTTCATGAAAGCCTTGAACACTCAATG
ACCGTCTGTTGGCGGTCTGCGGGCTGATATTCGAGTTGAGATGCCACGC 4200
AGACCGCCAACATGCGATGTATCATGTAAGTTAGATGAGTGACTGGCCAT
TGAGAAACGAGAGAAACAACCACTTCATGAGAGCCTTAAATTATTCAA 4300
TGACCAGTCTGTTACGGTCTGCGGGTTGGTATGCGAGTCGAGGTGCCTC
GCAGACCGCGAACATGCGATGTTTTCGATGGACGAGTGAAGCCTGACGAT 4400
CGAGAACTATCTCAGTTGGGTTGGCCATTCGGCTGGCCGTTGGGTTTAGT
ATTAGGATCGTCAGGTTTGTCCGATGGAACGTTCCGTTTGCGTGCGTTGG 4500
CGCGACGAGCCCTCTCCTCGGCGTGATTCTGAAATTCTGCAATCAGGGCA
GCCGCAGCACGGCGACGGGACGTCCTCCAGGAGCTGTGTTGAAGTTTCGG 4600
GGTGGCGGTCCAGAAGGGGGAGTTACATTAAAGCCTCATAGATGTCTTT
GGGTGGTTCGGGGGGGCCATCGCAAGATCTTCTGGAGTTGTGCGTCTGA 4700
TCATCTCTTGAGTGTAATTGCGACGCAGACCGAGCTTCAGGATTTTGGAA
GGGCTGGATCGCTCCTGCTGACTCTTCCCTCAGCGGGCTTCGTCTCGGC 4800
AGTCTTCATTTTCGGCGGGCTGATCTTCCATCTCAGAATGGGATCGCTTTC
TGGTCGCTGCACCCGCTCCTCCCTTCAAGGTCAGCTTGATGCGCAGCGTC 4900
TTGGGCGGCTCAGCTGGTGGAGTTGGTTCGGCTCTGGCTCCCTCCGGCG
TCGCTTGGGCACTTGAGTAGTCTCTGAGGCTTCGCCGCGCGCCGTTTGC 5000

Figure 6 (sheet 6 of 7)

GAGTCGGCTCCTTGGTCTCTTTGGCCTCTTTCACCTCACCTGGACCGTCT
TTCGGGGCGGTTTCATCGTGCTGAGCGATCAAGGTTTGGATGTAGGCAGC 5100
CGGCATCATTCGATCAACGGCAATTCCTCTCTTGCGGGCCTCCTCCCGAG
CCTTGATTGTGCGCTTGACCTCGTCCACGTTTTTCGAAGAAGAAAGGCATC 5200
TTGTTATCCTGAGGCAAGTTGCGCTCTCCCATGCGTGCGGATATCCGAAG
ATGCGGTCCTTCTCGAACTGTTTCATGAGACTTCAGACGAATTGGAGGCTG 5300
GGGAGCAATTTGTCTCCGTAGGTGTTGTTAGGGCGGAACCAAGAATAGC
CTTCGCCTACAACGACAAGCTCTTCGCCAAATTTATTTTTTTGGCCTGTA 5400
AAAACGAACCCATCCTCGTCAGTCCACCGGTGCGTCTCGGACGTAGAGAT
TGGCTTACTTATTCCCTCAACGCCGATCTCTGCCTGGGGCTGCGCTTCGG 5500
ATGCGGCCTCGGTACGGCTCCGCCTCGGACTGCACCGCTGGAGTTTCGG
TCTTCTTCTCCTGCTTCTCCAGGTACTCCTTGCGTAACTCTTCGATCAGC 5600
CTCGGCTTCCGATGACTGCTCAAATTCTGGAGCAACAGCTGCCGCGGCCA
GGTCAAGCAGGCGGTTTGCTAAAACTGCCCATTTTCCATCGACACCTGCC 5700
TCCGACGCCTGTGCAAAACCAGCTGTTTTTCGCATTGGCCTGTTTGTTGGC
ACGCGTCTTCTTGACTGCTGCCTTGCCCTTACTTCCTTGAGAGCAGACT 5800
CTGGCTTAGATGATGGTGCACGGTTTCTGCGGAAGCGCCGCTCAGATTCC
AAAGATTCCATAGCTTTAATGGTAGGCTTCTGGTTCTTCCAGAAGTGCG 5900
CGCAGCTGACGTAGTGGTTGAGTAGCTGGCAGTTGGGGATCCTGGGCCCT
CATTGGAACCATCAAGACCAATTTGTTTCCATACATATCAGCATGGTAT 6000

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— Figure 6 (sheet 7 of 7)

TCAAAGGAAACTTTCCCGGTACGGAGTACTGCGTTCGATTCCGGGTGT
ATCCAAGTCGTATCCAGACATGGTGTGAATTTCAGCCTTGCTGTCAAGAG 6100
CAGGGGTACTTTCAATGCTGTGAGCAACCACGCGGCCAAAGGGCGTCTTC
GGGAAAGAAGGTGTTTCAAGAGAAGCGTCATCCACGGCCTGGCTTGCGGC 6200
GTTGATTGCAGACTTTTCGAGTAGATCGCTGAGGTGCGGAAGTGGTTCGAG
TAGCAACCTGTGAATTGGCAGCCTTGTGACTGCTTCGATTCACTGCAGAG 6300
ACGGAGTAGACTGCACTGATTTGGAATTCTGAGTCGCAGCCATTCTGGAT
TTGCGTTCGGCGCGACGAGATCTCGCAGTCGTGGTACGAGGAGTAGAGCG 6400
AGGCTGCGTAGCAGTGTGCAAGCTTGGTGCTAGCCTCCTGGGCTTCAGC
AGCTTCAGCAGTGGTGGCAGACGCAGCAGAATTAGCGGAGCTTTATCGGC 6500
TTTGCGCTCTGAGCGTTGGGAGTAGAAGTGAGAGAAGAGGTAGAGTCCA
CGGAAGAAGTCTTCTCGCTGTTCTCAAAGCCGTTTCAGCTTTGCTGGCATA 6600
GACTTACGCGTCTTGCGGCTGTTGGAAGCGGAAGAGTTCATGGCGGGAGA
GGAGACGTTAGAAGTAGACATGGTGGGGTTTGTGACGGGTTTGTAGTAA 6700
CAAGAGACTTGCGTCGATCTTTGAGTGTTCTTGACAGAAAGTTATGCAAC

GTCGAC 6756
Sall

PHYTASE LOCUS

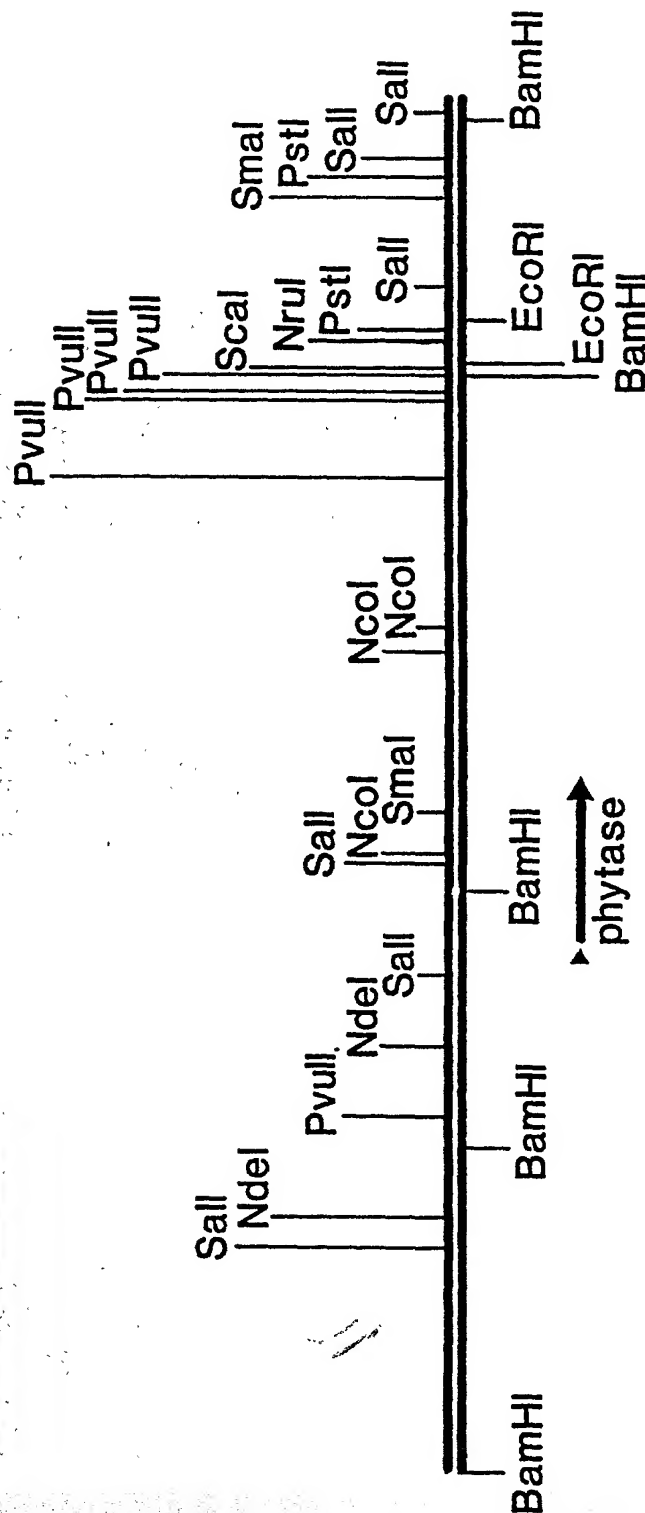


Figure 7

Figure 8 (sheet 1 of 2)

ATGGGGCGTCTCTGCTGTTCTACTTCCTTTGTATCTCCTGTCTGGAGTCAC
M G V S A V L L P L Y L L S G V T
-23 -20 -10

CTCCGGACTGGCAGTCCCCGCCTCGAGAAATCAATCCAGTTGCGATACGG 100
S G L A V P A S R N Q S S C D T
-1 +1 10

TCGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATCTTTGGGGTCAA
V D Q G Y Q C F S E T S H L W G Q
20

TACGCACCGTTCTTCTCTCTGGCAAACGAATCGGTCATCTCCCTGAGGT 200
Y A P F F S L A N E S V I S P E V
30 40

GCCCGCCGGATCGAGACTTCTGGCTCAGGTCCTCTCCCGTCATGGAG
P A G G R V T F A Q V L S R H G
50 60

CGCGGTATCCGACCGACTCCAAGGGCAAGAAATACTCCGCTCTCATTGAG 300
A R Y P T D S K G K K Y S A L I E
70

GAGATCCAGCAGAACGCGACCACCTTTGACGGAAAATATGCCTTCCTGAA
E I Q Q N A T T F D G K Y A F L K
80 90

GACATACAACCTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAAC 400
T Y N Y S L G A D D L T P F G E
100 110

AGGAGCTAGTCAACTCCGGCATCAAGTTCTACCAGCGGTACGAATCGCTC
Q E L V N S G I K F Y Q R Y E S L
120

ACAAGGAACATCGTTCCATTTCATCCGATCCTCTGGCTCCAGCCGCGTGAT 500
T R N I V P F I R S S G S S R V I
130 140

CGCCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGCACCAAGCTGAAGG
A S G K K F I E G F Q S T K L K
150 160

ATCCTCGTGCCCGAGCCCGGCCAATCGTCGCCCAAGATCGACGTGGTCATT 600
D P R A Q P G Q S S P K I D V V I
170

TCCGAGGCCAGCTCATCCAACAACACTCTCGACCCAGGCACCTGCACTGT
S E A S S S N N T L D P G T C T V
180 190

CTTCAAGACAGCGAATTGGCCGATACCGTCGAAGCCAATTTACCGCCA 700
F E D S E L A D T V E A N F T A
200 210

Figure 8 (sheet 2 of 2)

CGTTCGTCCCCTCCATTCGTCAACGTCTGGAGAACGACCTGTCCGGTGTG
T F V P S I R Q R L E N D L S G V
220

ACTCTCACAGACACAGAAGTGACCTACCTCATGGACATGTGCTCCTTCGA 800
T L T D T E V T Y L M D M C S F D
230 240

CACCATCTCCACCAGCACCGTCGACACCAAGCTGTCCCCCTTCTGTGACC
T I S T S T V D T K L S P F C D
250 260

TGTTACCCCATGACGAATGGATCAACCTACTAGCTCCAGTCCTTGAAA 900
L F T H D E W I N Y D Y L S L K
270

AAGTATTACGGCCATGGTGCAGGTAACCCGCTCGGCCCGACCCAGGGCGT
K Y Y G H G A G N P L G P T Q G V
280 290

CGGCTACGCTAACGAGCTCATCGCCCGTCTGACCCACTCGCCTGTCCACG 1000
G Y A N E L I A R L T H S P V H
300 310

ATGACACCAGTTCCAACCACACTTTGGACTCGAGCCCGGCTACCTTTCCG
D D T S S N H T L D S S P A T F P
320

CTCAACTCTACTCTCTACGCGGACTTTTCGCATGACAACGGCATCATCTC 1100
L N S T L Y A D F S H D N G I I S
330 340

CATTCTCTTACTTACGCTCTGTACAAACGGCACTAAGCCGCTATCTACCA
I L F A L G L Y N G T K P L S T
350 360

CGACCGTGGAGAATATCACCCAGACAGATGGATTCTCGTCTGCTTGGACG 1200
T T V E N I T Q T D G F S S A W T
370

GTTCCGTTTGCTTCGCGTTTGTACGTCGAGATGATGCAGTGTCAGGCGGA
V P F A S R L Y V E M M Q C Q A E
380 390

GCAGCAGCCGCTGGTCCGTGTCTTGGTTAATGATCGCGTTGTCCCGCTGC 1300
Q E P L V R V L V N D R V V P L
400 410

ATGGGTGTCCGGTTGATGCTTTGGGGAGATGTACCCGGGATAGCTTTGTG
H G C P V D A L G R C T R D S F V
420

AGGGGGTTGAGCTTTGCTAGATCTGGGGGTGATTGGGCGGAGTGTTTTCG 1400
R G L S F A R S G G D W A E C F A
430 440

TTAG 1404

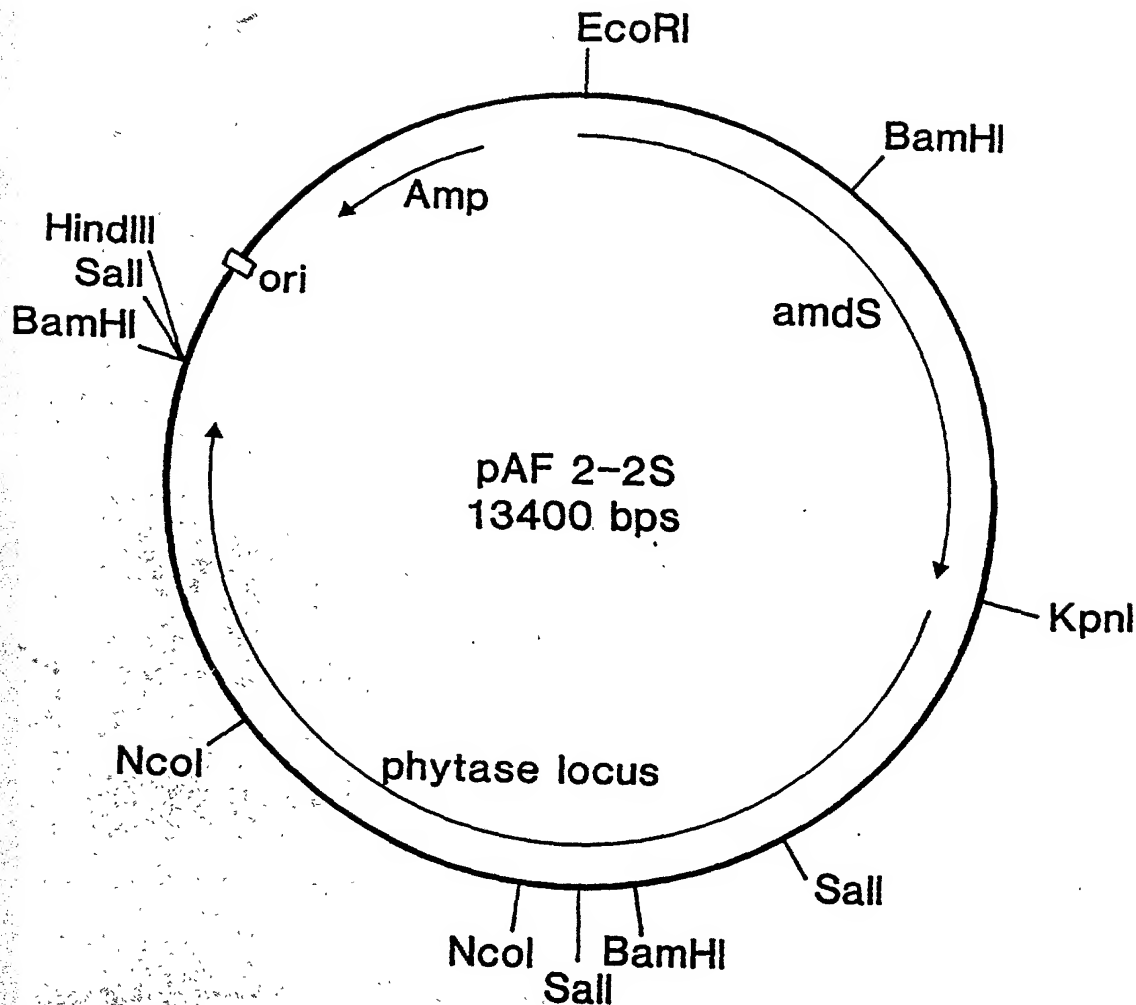


Figure 9

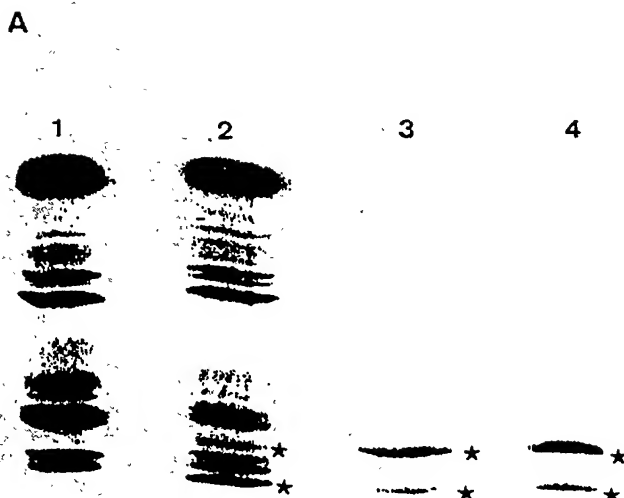


Figure 10a

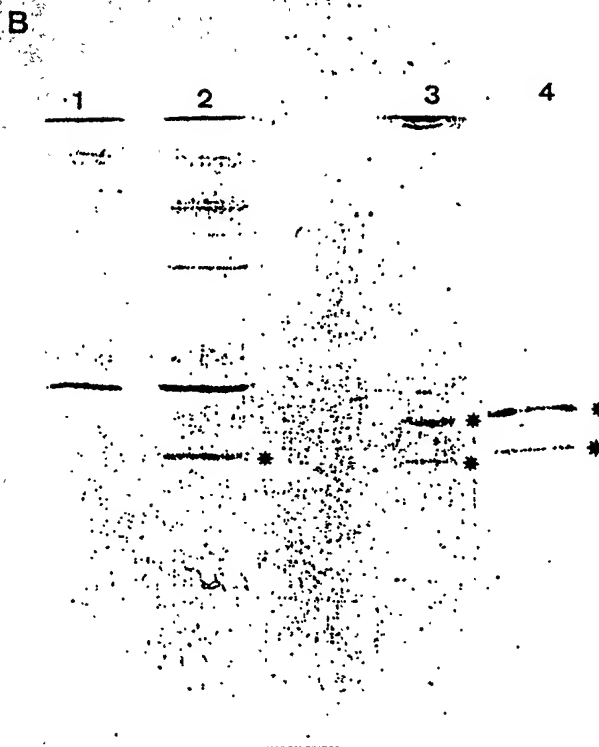


Figure 10b

A

1

2

3

4



Figure 11a

B

1

2

34

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Figure 11b

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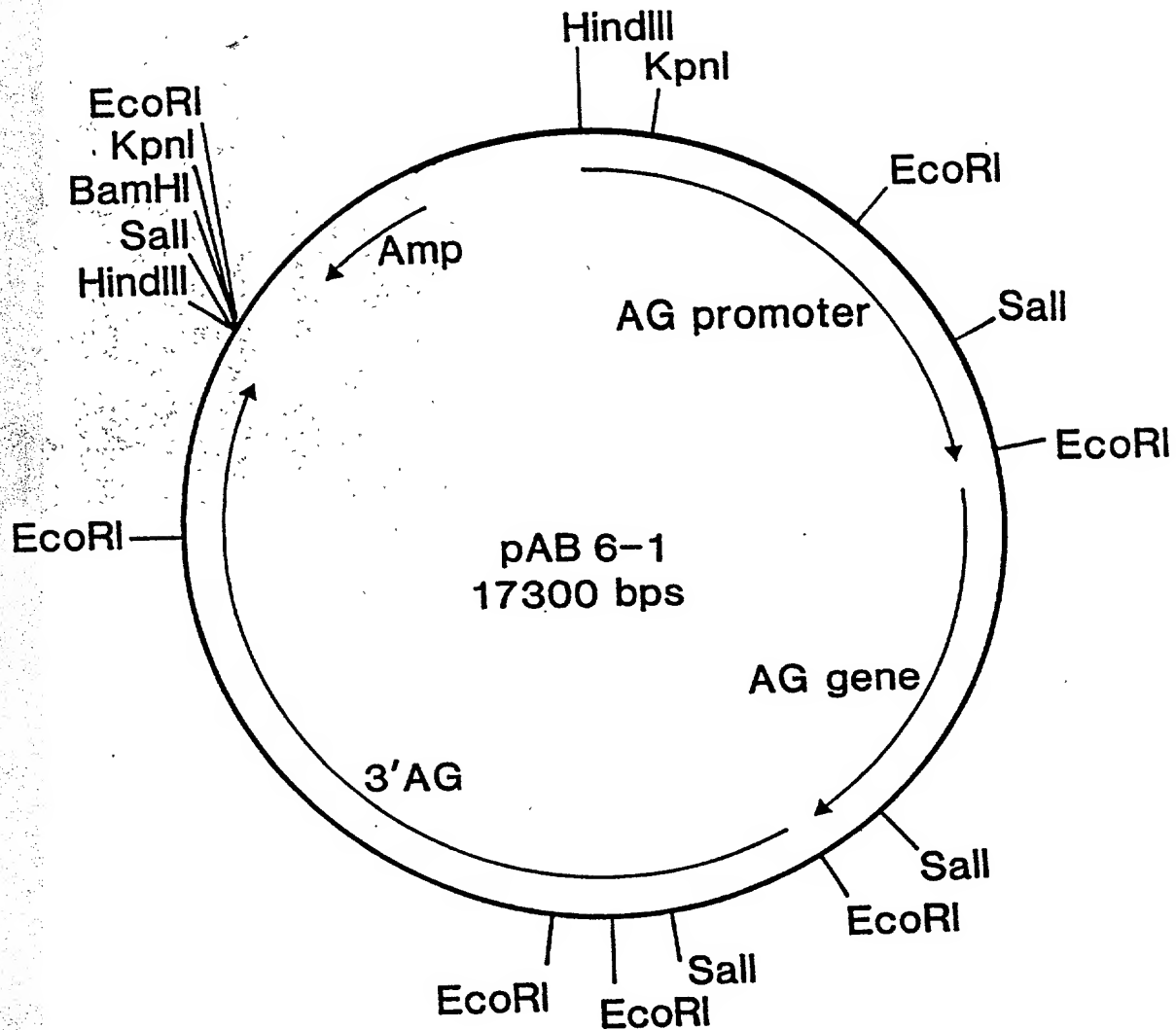


Figure 12

AG/PHTYASE GENE FUSIONS BY PCR

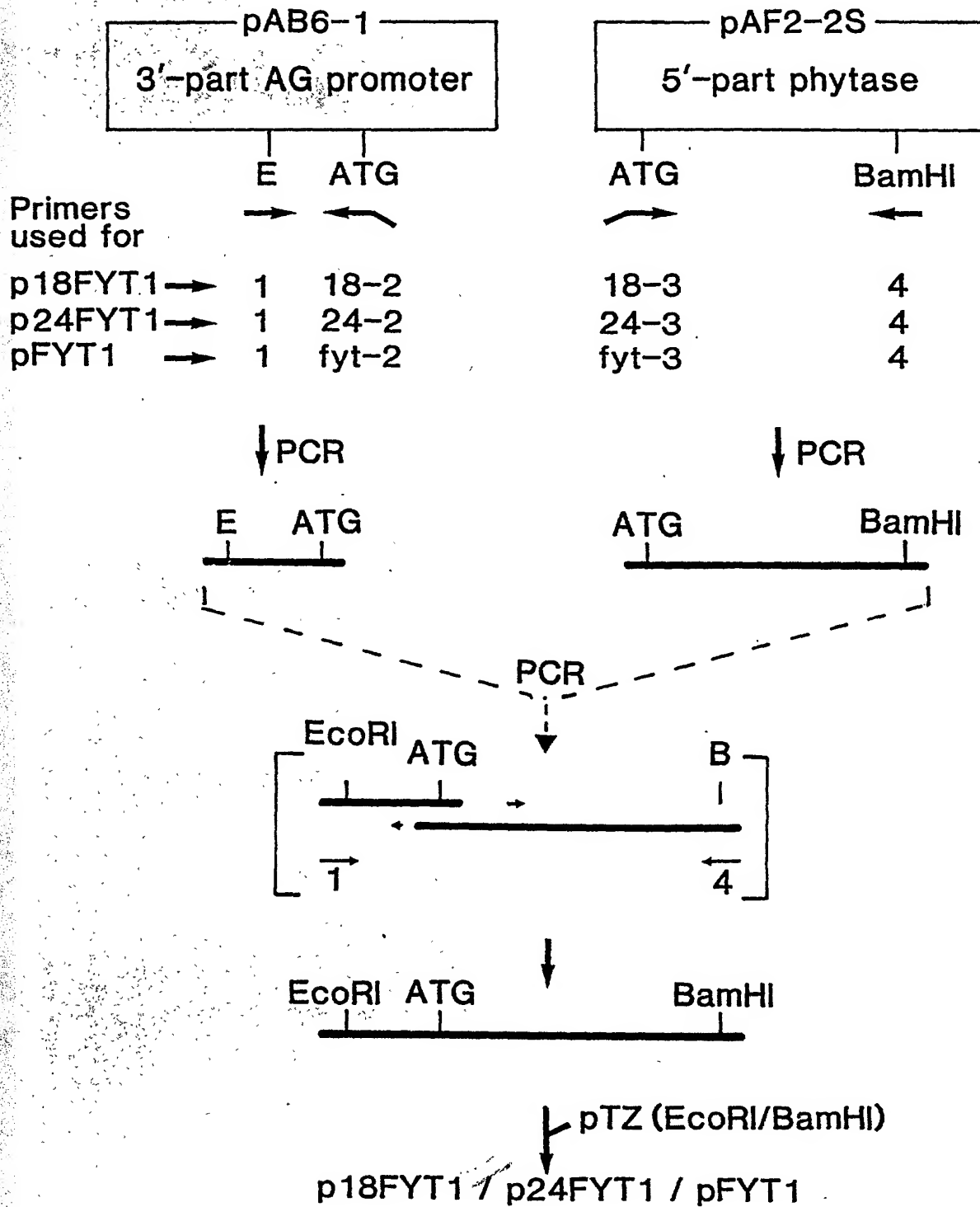


Figure 13

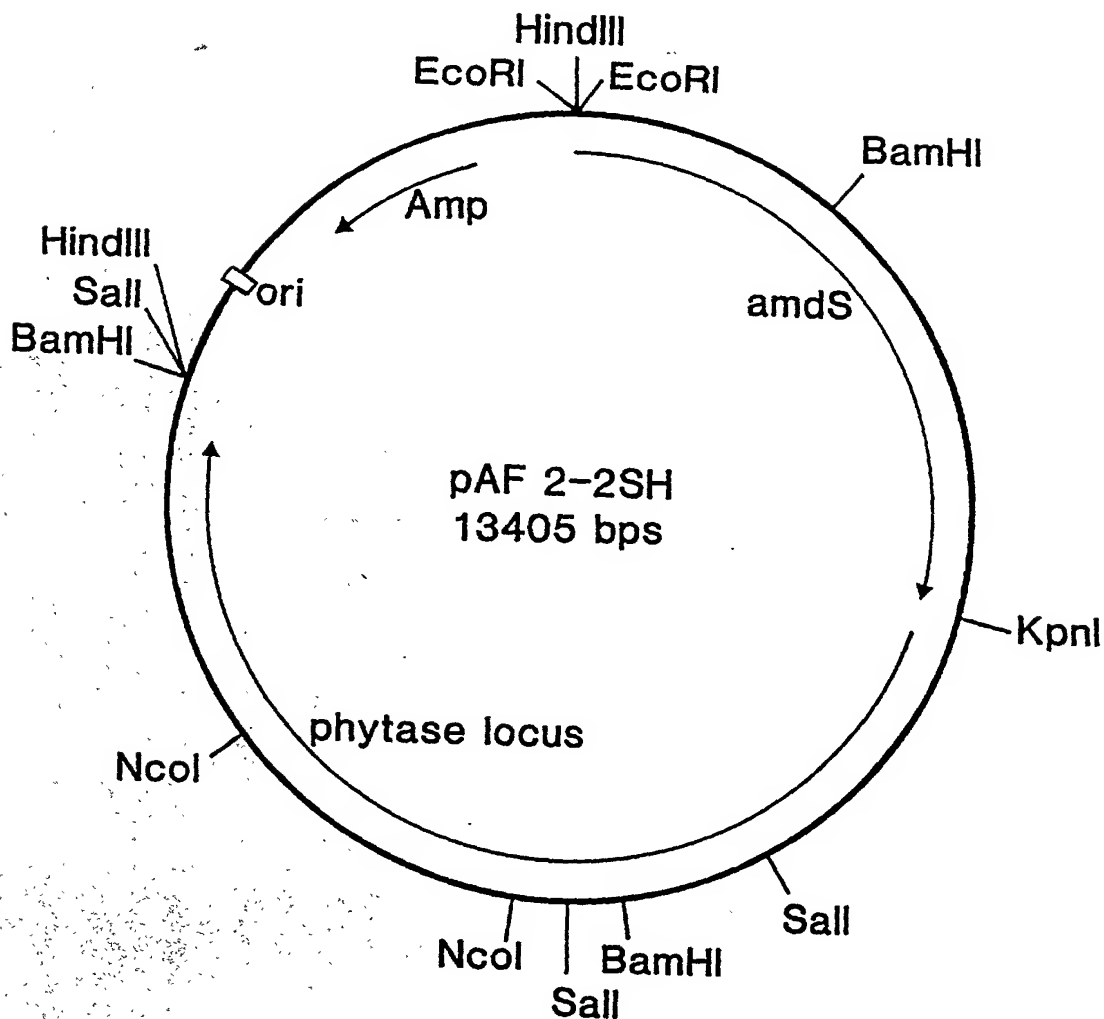


Figure 14

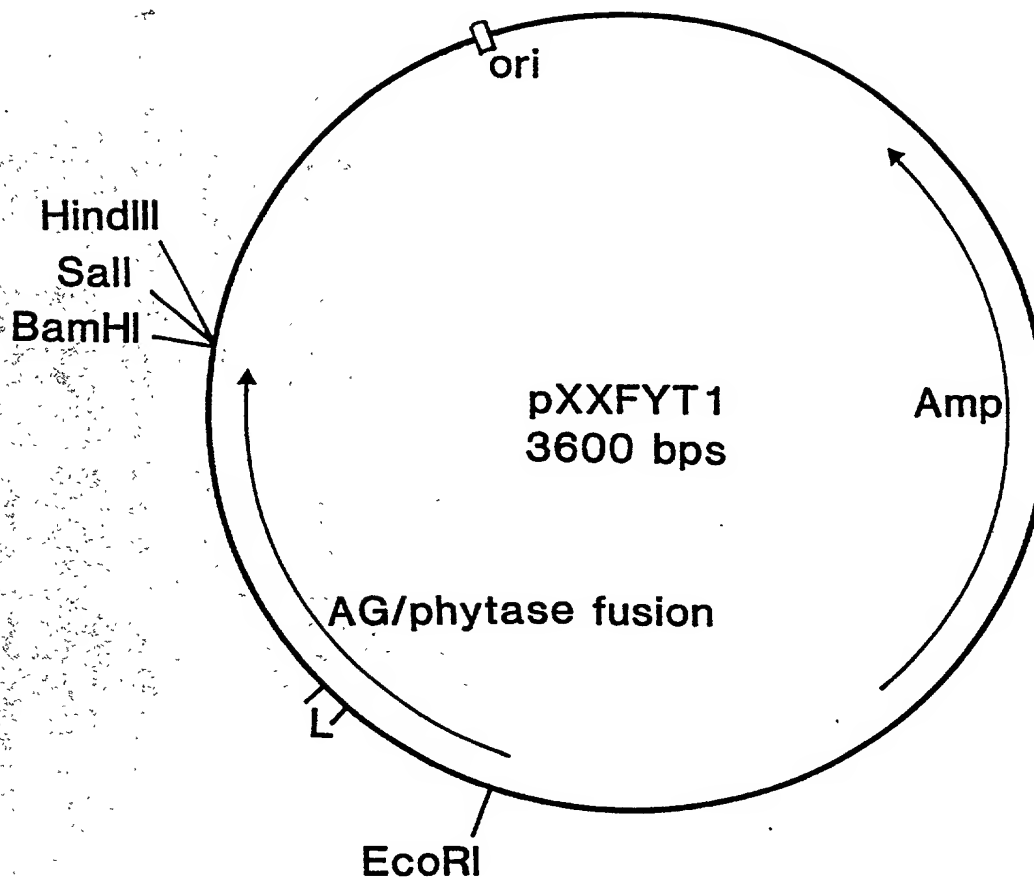


Figure 15a

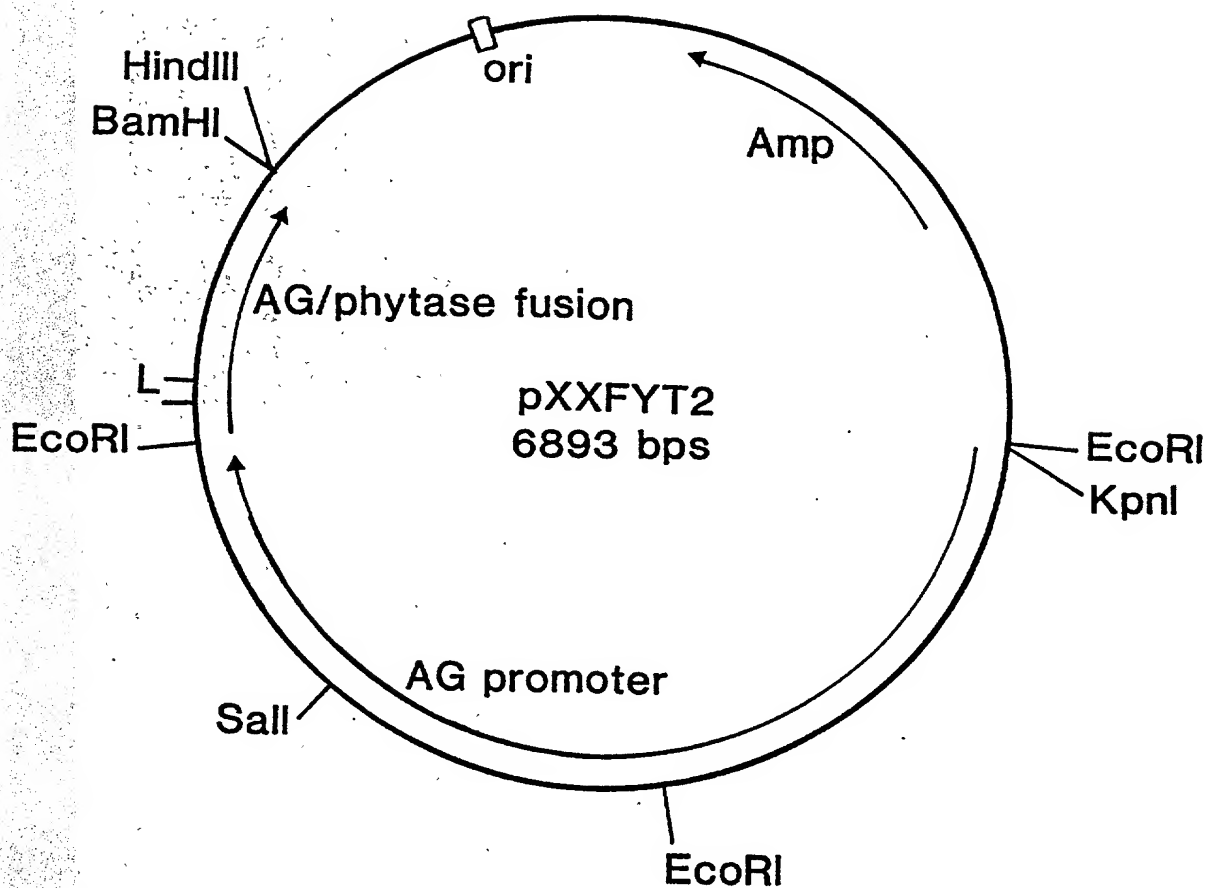


Figure 15b

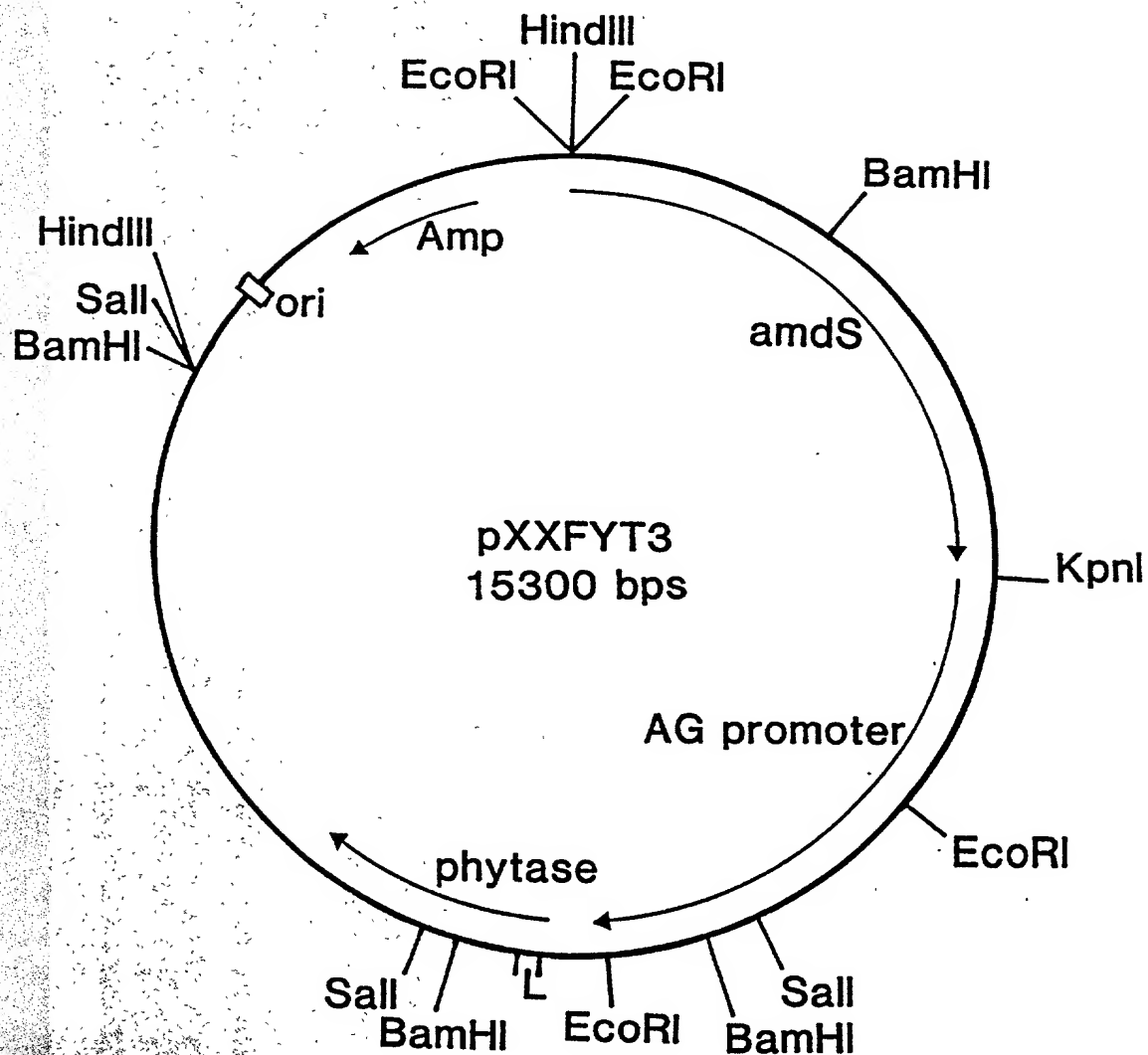


Figure 15c

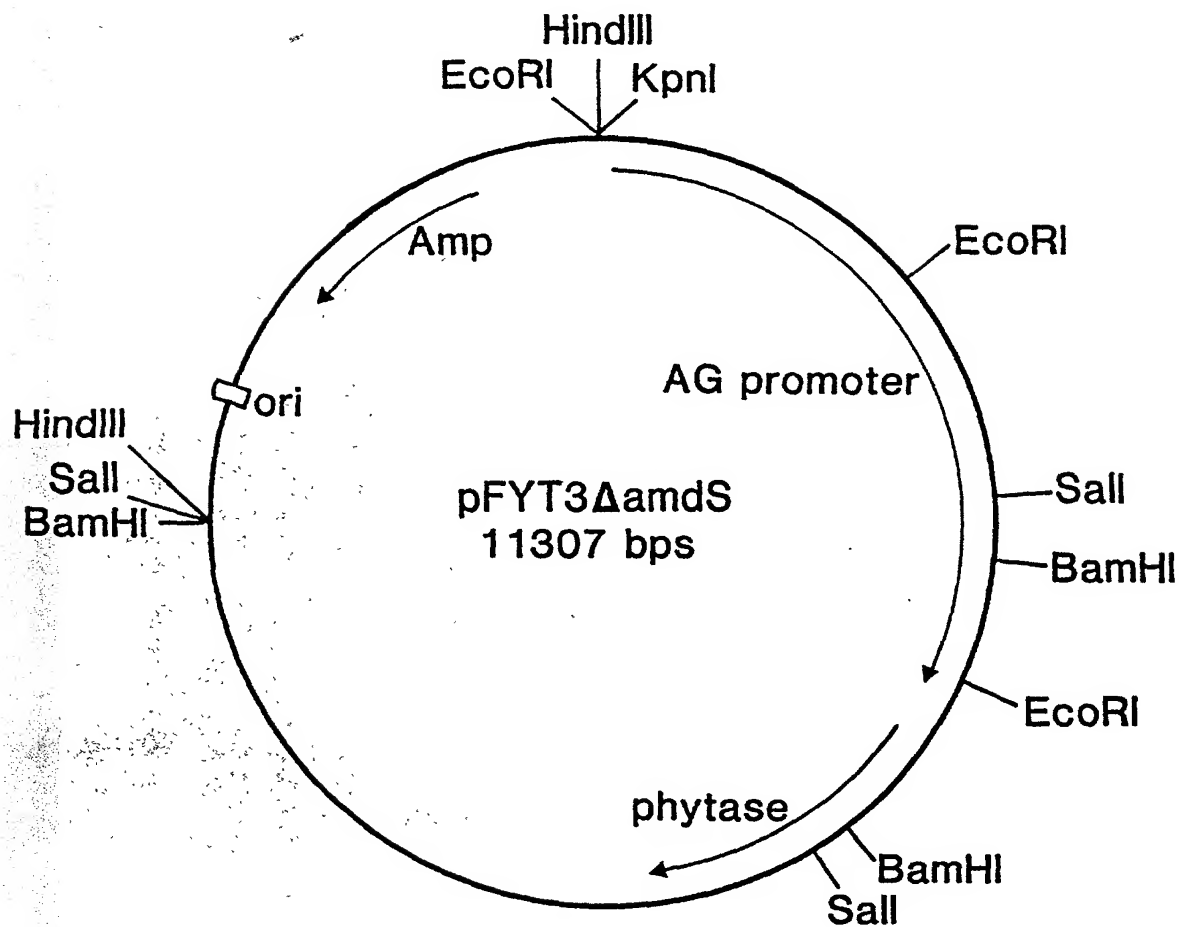


Figure 16

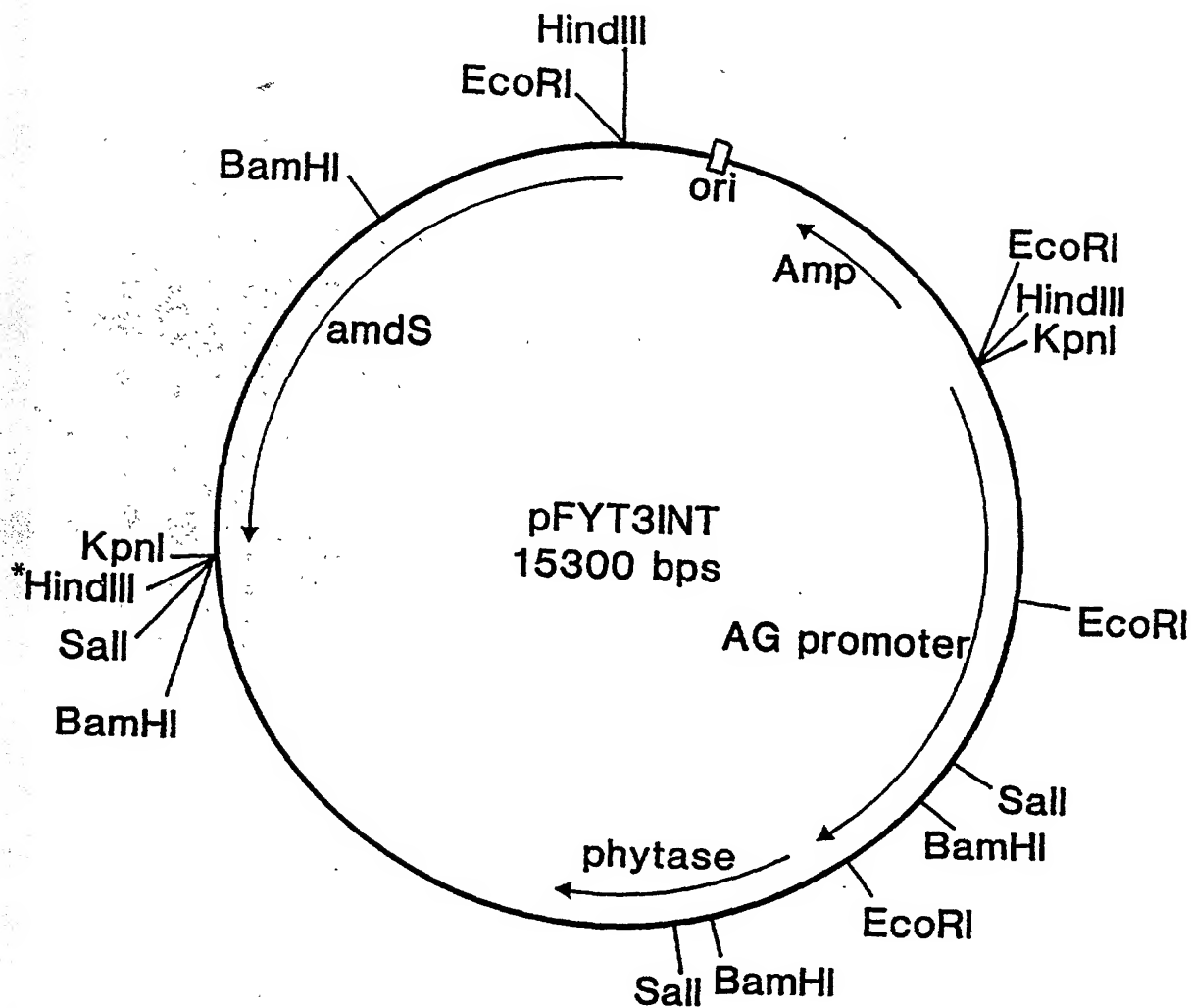


Figure 17

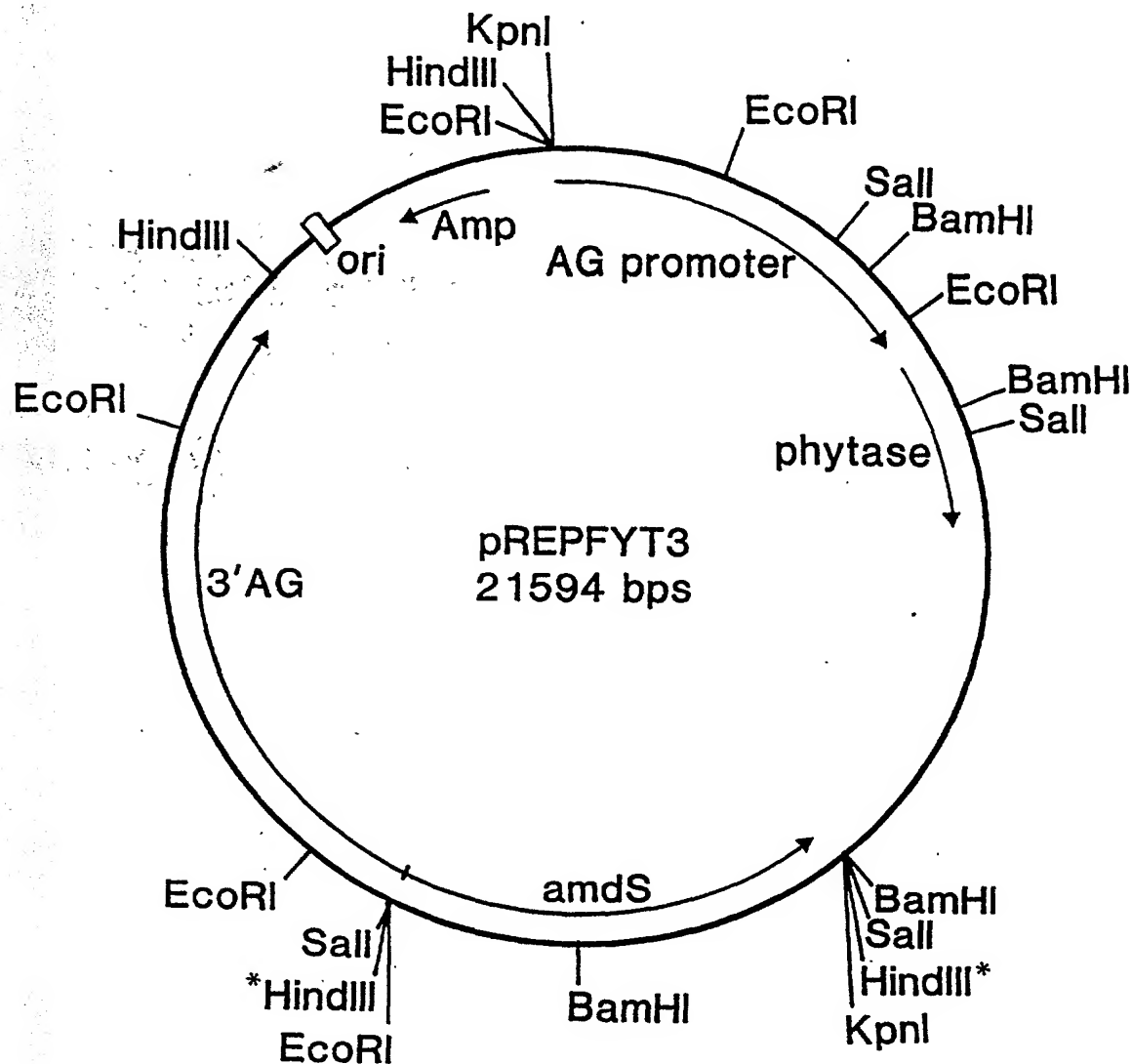


Figure 18

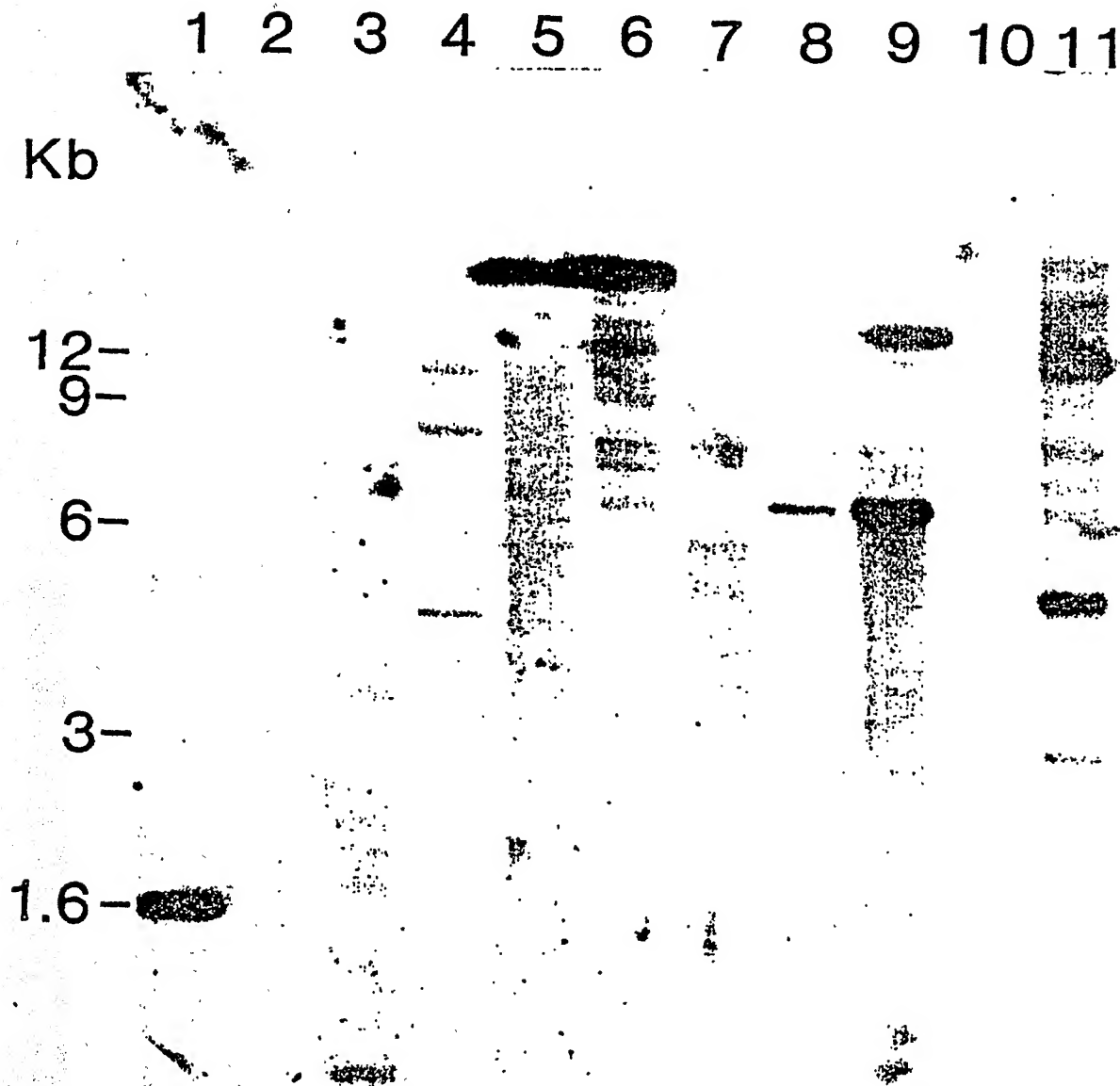


Figure 19a

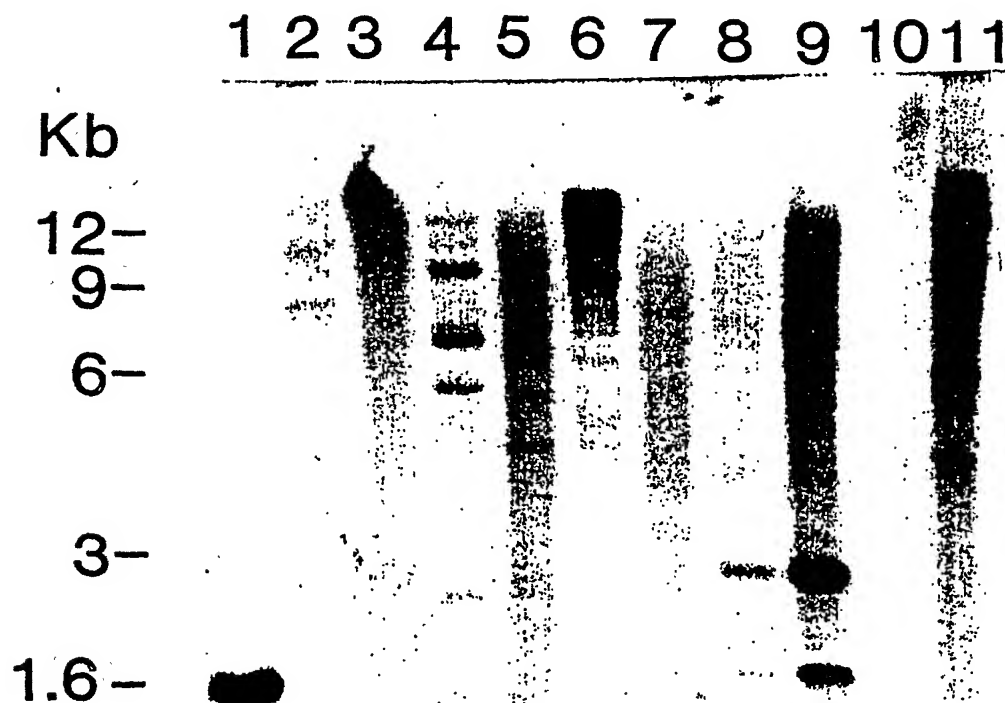


Figure 19b